

24. (New) An isolated polypeptide selected from the group consisting of:
- a) a polypeptide comprising an amino acid sequence of SEQ ID NO:1,
  - b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence of SEQ ID NO:1,
  - c) a biologically active fragment of a polypeptide having an amino acid sequence of SEQ ID NO:1, and
  - d) an immunogenic fragment of a polypeptide having an amino acid sequence of SEQ ID NO:1.

25. (New) An isolated polypeptide of claim 24 comprising an amino acid sequence of SEQ ID NO:1.

B) 26. (New) An isolated polynucleotide encoding a polypeptide of claim 24.

27. (New) An isolated polynucleotide encoding a polypeptide of claim 25.

28. (New) An isolated polynucleotide of claim 27 comprising a polynucleotide sequence of SEQ ID NO:2.

29. (New) A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 26.

30. (New) A cell transformed with a recombinant polynucleotide of claim 29.

31. (New) A method of producing a polypeptide of claim 24, the method comprising:

- a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant

polynucleotide comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 24, and

- b) recovering the polypeptide so expressed.

32. (New) A method of claim 9, wherein the polypeptide comprises an amino acid sequence of SEQ ID NO:1.

33. (New) An isolated polynucleotide selected from the group consisting of:

- a) a polynucleotide comprising a polynucleotide sequence of SEQ ID NO:2,
- b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence of SEQ ID NO:2,
- c) a polynucleotide complementary to a polynucleotide of a),
- d) a polynucleotide complementary to a polynucleotide of b), and
- e) an RNA equivalent of a)-d).

34. (New) An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 33.

35. (New) A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 33, the method comprising:

- a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and
- b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

36. (New) A method of claim 35, wherein the probe comprises at least 60 contiguous nucleotides.

37. (New) A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 33, the method comprising:

- a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and
- b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

B) 38. (New) A method of screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 27, the method comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,
- b) detecting altered expression of the target polynucleotide, and
- c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

39. (New) A method of assessing toxicity of a test compound, the method comprising:

- a) treating a biological sample containing nucleic acids with the test compound,
- b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 33 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 33 or fragment thereof,
- c) quantifying the amount of hybridization complex, and

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- d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.
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